

10/587956

IAP11 Rec'd PCT/PTO 31 JUL 2006

<110> Korea Research Institute of Bioscience and Biotechnology

<120> A novel Hansenula polymorpha gene coding for alpha 1,6  
mannosyltransferase and process for the production of recombinant  
glycoproteins with Hansenula polymorpha mutant strain deficient  
in the same gene

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<170> KopatentIn 1.71

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<211> 1351

<212> DNA

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<220>

<221> CDS

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gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc ccg ctg gtg 99  
Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val  
15 20 25 30

gtt gtt ctt gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg 147  
Val Val Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr  
35 40 45

tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag 195  
Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu  
50 55 60

gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac 243  
Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His  
65 70 75

tta aac cgg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc 291  
Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr  
80 85 90

ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg 339  
Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp  
95 100 105 110

cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac 387  
Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr  
115 120 125

aga cgg ttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac 435  
Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr  
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cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr 145 150 155	483
gcg aac gtg ccg gag gtg gtc aga gcg tac cag ctg ctt ccg aaa aat Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn 160 165 170	531
atc atg aag gcg gat ttt ttc cgg tat ttg gtg atc tac gcg cgc gga Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly 175 180 185 190	579
ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp 195 200 205	627
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gat ctc tcc cag ata gat cca gaa gca aga acc acg cct gtg ggg ctg Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu 225 230 235	723
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act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly 320 325 330	1011
gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr 335 340 345 350	1059
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gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca	1155

Glu Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro			
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Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro			
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Asn Val Gly His Met Gly Ser Lys Ser Ser Asp Arg Leu Ala Phe			
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Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu			
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Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His Leu Asn			
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Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr Phe Tyr			
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Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp Gln Thr			
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Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr Arg Arg			
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Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr His Leu			
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Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr Ala Asn			
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Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn Ile Met			
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Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly Gly Thr  
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Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp Trp Ala  
195 200 205

Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala Asp Leu  
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Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu Val Ile  
225 230 235 240

Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp Phe Ser  
245 250 255

Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro Gly His  
260 265 270

Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr Phe Arg  
275 280 285

Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp Ser Gly  
290 295 300

Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp Thr Leu  
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Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly Asp Gly  
325 330 335

Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr Lys Leu  
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Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser Glu Asp  
355 360 365

Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro Lys Ile  
370 375 380

Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro Asn Val  
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His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys  
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